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ER 1600300

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/435,770 A

Source: 1652

Date Processed by STIC: 3-30-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/435,770

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 J Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 J Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,770A

DATE: 03/30/2001

TIME: 10:46:41

Input Set : A:\YAMAMTO1.txt

Output Set: N:\CRF3\03302001\I435770A.raw

Does Not Comply
Corrected Diskette Needed
See pp. 1-4

4 <110> APPLICANT: YAMAMOTO, Takuo
5 MARUTA, Kazuhiko
6 KUBOTA, Michio
7 FUKUDA, Shigeharu
8 MIYAKE, Toshio
10 <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,
11 TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
12 SACCHARIDES USING THE ENZYMES
14 <130> FILE REFERENCE: YAMAMOTO=16A
16 <140> CURRENT APPLICATION NUMBER: 09/435,770A
17 <141> CURRENT FILING DATE: 1999-11-08
19 <150> PRIOR APPLICATION NUMBER: JP 258,394/1998
20 <151> PRIOR FILING DATE: 1998-09-11
22 <150> PRIOR APPLICATION NUMBER: JP 352,252/1998
23 <151> PRIOR FILING DATE: 1998-12-11
25 <150> PRIOR APPLICATION NUMBER: JP 16,931/1999
26 <151> PRIOR FILING DATE: 1999-01-26
28 <160> NUMBER OF SEQ ID NOS: 39
30 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

286 <210> SEQ ID NO: 8
287 <211> LENGTH: 28
288 <212> TYPE: DNA
289 <213> ORGANISM: ARTHROBACTER sp.S34
291 <400> SEQUENCE: 8
E--> 292 tttttaata aaatcaggag gaaaaaat
293 (28) → "wrapped" nucleic acid number. Move to end of nucleic line.
913 <210> SEQ ID NO: (32)
914 <211> LENGTH: 2218
915 <212> TYPE: DNA
916 <213> ORGANISM: Artificial Sequence
918 <220> FEATURE:
919 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
921 <220> FEATURE:
922 <221> NAME/KEY: CDS
923 <222> LOCATION: (477)..(2201)
925 <220> FEATURE:
926 <221> NAME/KEY: 3'UTR
927 <222> LOCATION: (2202)..(2218) → Sequence # 32?
E--> 929 <400> SEQUENCE: (33)
930 ctgcagctgc tcgcccccggt aacccccgac gtgtaccagg gcacggaacg ctgggaccgg 60
932 togtctggtgg acccggaaca ccgtcgcccc gtggatttcg ccgcggcatc cgagctgctc 120
934 gaccgctctg acggcggtcg gcgccgcgcc gtgcacgaga ccggcgcggt caagacgctc 180
936 gtcgtctccc gcgcgctgcg gctgcgcgcg gaccggcccg agctgttcac cgcgtaccac 240

RAW SEQUENCE LISTING

DATE: 03/30/2001

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TIME: 10:46:41

Input Set : A:\YAMAMT01.txt

Output Set: N:\CRF3\03302001\I435770A.raw

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938 ccggtcacgg cgcgcggcgc gcaggccgag cacctgatcg gcttcgaccg cggcggcgcg 300
940 atcgccctgg ccacccgcct gccgctcggc ctgcgcgcgc caggcggctg gggcgacacg 360
942 gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccgcgga 420
944 gcggcgcgcg tggccgagtt gttcgccgac taccocgtcg ccctgctggt ggagac atg 479
945 Met
946 1
948 aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc 527
949 Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu
950 5 10 15
952 gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac 575
953 Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn
954 20 25 30
956 gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc 623
957 Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val
958 35 40 45
960 gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg 671
961 Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg
962 50 55 60 65
964 tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac 719
965 Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp
966 70 75 80
968 ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc 767
969 Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu
970 85 90 95
972 acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag 815
973 Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu
974 100 105 110
976 gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc 863
977 Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu
978 115 120 125
980 ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc 911
981 Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr
982 130 135 140 145
984 cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc 959
985 His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro
986 150 155 160
988 tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc 1007
989 Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His Ala
990 165 170 175
992 cgc ggc ctc gcc gtc gtg cag gac gtc gtc tac aac cac ctg ggc ccg 1055
993 Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly Pro
994 180 185 190
996 agc ggc aac cac ctg ccc gac ttc ggc ccc tac ctc ggg tcg ggc gcc 1103
997 Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly Ala
998 195 200 205
1000 gcc aac acc tgg ggc gac gcg ctg aac ctc gac ggg ccg ctc tcc gac 1151
1001 Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser Asp
1002 210 215 220 225
1004 gag gtg cgg cgg tac atc atc gac aac gcg gtg tac tgg ctg cgc gac 1199

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RAW SEQUENCE LISTING

DATE: 03/30/2001

PATENT APPLICATION: US/09/435,770A

TIME: 10:46:41

Input Set : A:\YAMAMTO1.txt

Output Set: N:\CRF3\03302001\I435770A.raw

```

1005 Glu Val Arg Arg Tyr Ile Ile Asp Asn Ala Val Tyr Trp Leu Arg Asp
1006                230                235                240
1008 atg cac gcc gac ggg ctg cgg ctc gac gcc gtg cac gcg ctg cgc gac 1247
1009 Met His Ala Asp Gly Leu Arg Leu Asp Ala Val His Ala Leu Arg Asp
1010                245                250                255
1012 gcc cgc gcg ctg cac ctg ctc gaa gag ctc gcc gcc cgc gtc gac gag 1295
1013 Ala Arg Ala Leu His Leu Leu Glu Glu Leu Ala Ala Arg Val Asp Glu
1014                260                265                270
1016 ctg gcg ggc gag ctc ggc cgg ccg ctg acg ctc atc gcc gag agc gac 1343
1017 Leu Ala Gly Glu Leu Gly Arg Pro Leu Thr Leu Ile Ala Glu Ser Asp
1018                275                280                285
1020 ctg aac gac ccg aag ctg atc cgc tcc cgc gcg gcg cac ggc tac ggc 1391
1021 Leu Asn Asp Pro Lys Leu Ile Arg Ser Arg Ala Ala His Gly Tyr Gly
1022 290                295                300                305
1024 ctc gac gcc cag tgg gac gac gac gtg cac cac gcg gtg cac gcc aac 1439
1025 Leu Asp Ala Gln Trp Asp Asp Asp Val His His Ala Val His Ala Asn
1026                310                315                320
1028 gtg acc ggc gag acc gtc ggc tac tac gcc gac ttc ggc ggg ctc ggc 1487
1029 Val Thr Gly Glu Thr Val Gly Tyr Tyr Ala Asp Phe Gly Gly Leu Gly
1030                325                330                335
1032 gcc ctc gtc aag gtg ttc cag cgc ggc tgg ttc cac gac ggc acc tgg 1535
1033 Ala Leu Val Lys Val Phe Gln Arg Gly Trp Phe His Asp Gly Thr Trp
1034                340                345                350
1036 tcg agc ttc cgc gag cgg cac cac ggc cgg ccg ctc gac ccc gac atc 1583
1037 Ser Ser Phe Arg Glu Arg His His Gly Arg Pro Leu Asp Pro Asp Ile
1038                355                360                365
1040 ccg ttc cgc cgg ctc gtc gcc ttc gcg cag gat cac gac cag gtc ggc 1631
1041 Pro Phe Arg Arg Leu Val Ala Phe Ala Gln Asp His Asp Gln Val Gly
1042 370                375                380                385
1044 aac cga gcg gtc ggc gac cgc atg tcg gcg cag gtc ggc gag ggt tcg 1679
1045 Asn Arg Ala Val Gly Asp Arg Met Ser Ala Gln Val Gly Glu Gly Ser
1046                390                395                400
1048 ctc gcc gcc gcg gcg gcg ctc gtg ctg ctc ggc ccg ttc acc ccg atg 1727
1049 Leu Ala Ala Ala Ala Ala Leu Val Leu Leu Gly Pro Phe Thr Pro Met
1050                405                410                415
1052 ctg ttc atg ggc gag gag tgg ggc gcg cgc acc ccg tgg cag ttc ttc 1775
1053 Leu Phe Met Gly Glu Glu Trp Gly Ala Arg Thr Pro Trp Gln Phe Phe
1054                420                425                430
1056 acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc 1823
1057 Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg
1058                435                440                445
1060 atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac 1871
1061 Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp
1062 450                455                460                465
1064 ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag 1919
1065 Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu
1066                470                475                480
1068 ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg 1967
1069 Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu

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Input Set : A:\YAMAMTO1.txt

Output Set: N:\CRF3\03302001\I435770A.raw

```

1070          485          490          495
1072 atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtg 2015
1073 Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val
1074          500          505          510
1076 gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg 2063
1077 Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu
1078          515          520          525
1080 cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac 2111
1081 Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His
1082 530          535          540          545
1084 ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gcc gga 2159
1085 Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly
1086          550          555          560
1088 ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag 2201
1089 Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu
1090          565          570          575
1092 tgacgcggct gggtacc 2218
1166 <210> SEQ ID NO: 39
1167 <211> LENGTH: 22
1168 <212> TYPE: DNA
1169 <213> ORGANISM: Artificial Sequence
1171 <220> FEATURE:
1172 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
1174 <400> SEQUENCE: 39
1175 aggtggttgt agacgacgtc ct 22

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E--> 1181 20
E--> 1187 15

→ Delete extraneous numerals from the end of the file. They are causing an invalid base count for sequence #39.

VERIFICATION SUMMARY

DATE: 03/30/2001

PATENT APPLICATION: US/09/435,770A

TIME: 10:46:42

Input Set : A:\YAMAMT01.txt

Output Set: N:\CRF3\03302001\I435770A.raw

L:292 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:8
L:909 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:909 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:929 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:33
L:1181 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:22 SEQ:39
M:254 Repeated in SeqNo=39